Notice of the Final Oral Examination
for the Degree of Doctor of Philosophy

of

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BSc (University of Washington, 1998)

“Relating prokaryotic and microeukaryotic diversity to community function and ecosystem variability at deep-sea hydrothermal vents”

School of Earth and Ocean Sciences

Tuesday, June 8, 2021
8:00 A.M.
Conducted Virtually

Supervisory Committee:
Dr. Kim Juniper, School of Earth and Ocean Sciences, University of Victoria (Supervisor)
Dr. John Dower, School of Earth and Ocean Sciences, UVic (Member)
Dr. Connie Lovejoy, Département de biologie, Université Laval (Outside Member)
Dr. Verena Tunnicliffe, Department of Biology, UVic (Outside Member)

External Examiner:
Dr. Marie-Anne Cambon-Bonavita, Research Scientist, Institut français de recherche pour l'exploitation de la mer (IFREMER)

Chair of Oral Examination:
Dr. Jeremy Wulff, Department of Chemistry, UVic

Dr. Stephen Evans, Acting Dean, Faculty of Graduate Studies
Abstract
Despite over four decades of research on deep-sea hydrothermal vent ecosystems, major gaps remain in our understanding of these systems. Knowledge of microeukaryote diversity, abundance, and involvement in ecosystem function lag far behind that of prokaryotes. Contributions of faunal assemblage microbes to ecosystem processes and overall hydrothermal vent microbial diversity are not known. This research addresses these gaps using high-throughput sequencing of 16S/18S rRNA genes and metagenomes from vent and non-vent habitats encompassing diffuse hydrothermal fluids, plumes, deep seawater, and microbes in assemblages of the foundation tubeworm species Ridgeia piscesae. Cooccurrence/covariance is a central method used, first, between prokaryotes with known extreme habitat preferences and microeukaryotes to infer potential endemism in the latter, and then between microbes and fauna in R. piscesae assemblages to infer interspecies interactions. Microeukaryote distribution and abundance suggest potential vent endemic microeukarya are infrequently encountered, potentially in low abundance, and belong to novel lineages of Rhizaria and Stramenopila. Potential endemism is inferred for relatives of known apusomonads, excavates, and some clades of Syndiniales. R. piscesae assemblages are hotspots of microbial taxonomic richness and exhibited a robust temperature-driven distinction in assemblage composition above and below ~25°C that spanned size classes and microbial domains. Likely interacting faunal and microbial taxa among R. piscesae assemblages are identified as ‘core communities’ and used to guide metagenomics investigations of microbial functional potential. Exploratory metagenomic analysis revealed clades within core community microbes with differing functional potential between highT and lowT assemblages and between assemblages and fluids. Community functional metrics including the balance of autotrohy-heterotrohy genes and genes involved in different carbon, nitrogen, and sulfur-cycling processes are tested. Combined results help to fill some of the gaps in knowledge of hydrothermal vent ecosystem function and suggest sizeable continued discovery potential.